

REMARKS/ARGUMENTS

Claims 1-28 remain pending.

Regarding the Restriction Requirement, Applicants elect, with traverse, Group VII: Claims 14, 15, 17-21, and 23-28. The elected claims are directed to a vector comprising a DNA sequence encoding a protein or a peptide, to methods of transforming plant cells, and to plants and plant materials. Applicants also elect, for initial examination purposes only, (A) SEQ ID NO: 6.

Applicants explicitly request that non-elected Groups I and V be rejoined with elected Group VII.

Group I is Claims 1-4 and 7, directed to at least partially purified protein or peptide. Group V is Claims 10-13, directed to non-genomic DNA sequences a protein or a peptide.

Restriction is proper only when (1) the inventions are independent or distinct and (2) there is a serious burden on the Examiner in the absence of restriction. MPEP §803.

The case for rejoining Group V with Group VII is particularly strong. Group V is directed to a DNA coding for a specified product. See Claim 10. Group VII is directed to a vector which comprises the DNA of Group V. In fact, Claim 14 in Group VII depends directly from Claim 10. Therefore, the search and examination for elected Group VII will necessarily require a search and examination for non-elected Group V. Certainly, there is no serious burden on the Examiner in this situation. Accordingly, restriction between Group V and Group VII is not proper. Those Groups should be rejoined.

While Group I is directed to materials comprised of amino acids, the search and examination required for Groups V and VII will overlap with that required for Group I such that the Examiner will not be seriously burdened. Therefore, restriction between Group I and VII is improper. Accordingly, Group I should also be rejoined with Group VII.

The requirement for an election of one of species (A)-(J) is also traversed. MPEP

§803.04 reads in pertinent part:

Nevertheless, to further aid the biotechnology industry in protecting its intellectual property without creating an undue burden on the Office, the Commissioner has decided *sua sponte* to partially waive the requirements of 37 C.F.R. § 1.141 *et seq.* and permit a reasonable number of such nucleotide sequences to be claimed in a single application. See *Examination of Patent Applications Containing Nucleotide Sequences*, 1192 O.G. 68 (November 19, 1996).

It has been determined that normally ten sequences constitute a reasonable number for examination purposes. Accordingly, in most cases, up to ten independent and distinct nucleotide sequences will be examined in a single application without restriction. In addition to the specifically selected sequences, those sequences which are patentably indistinct from the selected sequences will also be examined. Furthermore, nucleotide sequences encoding the same protein are not considered to be independent and distinct inventions and will continue to be examined together. Only the ten nucleotide sequences selected in response to the restriction requirement and any other claimed sequences which are patentably indistinct therefrom will be examined.

Only the ten nucleotide sequences selected in response to the restriction requirement...will be examined. [Emphasis added.]

Since the MPEP explicitly prescribes the examination of up to 10 sequences, Applicants respectfully request that sequences (A)-(J), i.e., 10 sequences, be examined in this application without restriction. The Office has given no reason whatsoever why the procedure explicitly provided for in the MPEP should not be followed in the present application.

Moreover, SEQ ID NO's (A)-(J) are capable of use together. The Examiner considers (A) to (J) unrelated inventions because in hybridization experiments they would give a different result. However, Applicants submit that "hybridization experiments" are not a main feature of the present invention. A main feature of the present invention is a method to improve the phenotype of plants, especially to improve the growth of the cells (see paragraph

94 at pages 25 and 26 of the specification). Applicants note that if any of the sequences (A)-(J) are used in the methods of the present invention, they would all behave in the same way. Moreover, even for hybridization experiments, the sequences can be used to obtain the same effect, i.e., to hybridize with cdc27 proteins.

The Examiner alleges that because the proteins are structurally different, they have different effects, but Applicants believe that there is no proof for this. If the Examiner maintains that opinion, Applicants respectfully request that supportive proof be provided which demonstrates that the sequences of (A)-(J) would have different effects. Contrarily, there is a substantially sequence identity and sequence similarity between the claimed proteins and genes and we have evidence that several of them are useful for making transgenic plants with improved phenotypic characteristics. It is precisely because the sequences (A)-(J) refer to proteins of the same genus, they will have the same effects, as has been found by the present inventors.

Applicants note that the reasoning at page 4, line 11, of the Restriction Requirement is incorrect because the different groups (A)-(J) represent the same class of proteins, namely cdc27 proteins. See the following Table. Since the claimed proteins and genes belong to the same genus, namely cdc27 proteins and encoding genes, Applicants believe that the present Restriction Requirement as an unjust obligation to choose a single member species from a genus of proteins and genes. Applicants respectfully assert that they are entitled to this genus of plant proteins since the inventors were the first to isolate cdc27 proteins as claimed.

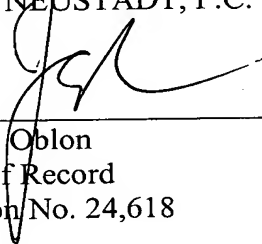
SEQ ID NO	GROUP	
6	A	First exon of cdc27 (forms part of natural cdc27 proteins)
7	B	Last exon of cdc27 (forms part of natural cdc27 proteins)
5	E	Amino acid sequence of cdc27A protein (1 possible allele)
11	F	Amino acid sequence of cdc27A protein (another possible allele)
13	G	Amino acid sequence of cdc27B protein
9	H	CDNA encoding SEQ ID NO 5
14	I	CDNA encoding SEQ ID NO 9
15	J	CDNA encoding SEQ ID NO 13

Moreover, the reasoning at page 4, line 13, of the Restriction Requirement is not correct because all the sequences of inventions (A)-(J) as claimed refer to a novel genus of proteins, namely plant cdc27 proteins. The claims of elected Group VII (methods to transform plants and plants), recite different sequences with the same effect, namely that they alter the plant's phenotype.

Applicants submit that the present application is ready for examination on the merits. Early notice to this effect is earnestly solicited.

Respectfully submitted,

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